

57661
SEARCH REQUEST FORM

Requestor's

Name: Bronwen Loeb

Serial

Number: 09/635,521Date: 1/7/02Phone: 605-1197Art Unit: 1636MAILBOX: 11 E 12OFFICE: 12 D 12**Search Topic:**

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

Please search the commercial
nucleotide databases for Seq ID No. 1
and the commercial protein databases
for Seq ID No. 2

Edward Hart
Technical Info Specialist
STIC / Biotech
CM1 12C14 Tel: 305-9203

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Searcher: _____

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Total time: _____

Number of Searches: _____

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Search Site

☒ STIC☒ CM-1☐ Pre-S

Type of Search

☒ N.A. Sequence☒ A.A. Sequence☐ Structure☐ Bibliographic

Vendors

☐ IG☐ STN☐ Dialog☐ APS☐ Geninfo☐ SDC☐ DARC/Questel☒ Other

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 8, 2002, 23:04:10 ; Search time 24.21 Seconds
(without alignments) 686.046 Million cell updates/sec

Title: US-09-635-521A-2

Perfect score: 2334
Sequence: 1 MASPSLPGSDCSQIIDHSV.....NSGAKPANSALNGFQEHYV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 segs, 36664827 residues

Number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23.4	100.0	453	1	GP39_HUMAN
2	481.5	20.6	424	1	NPRL_MOUSE
3	473	20.3	424	1	NPRL_RAT
4	466.5	20.0	418	1	NPRL_HUMAN
5	419	18.0	416	1	NPRL_RAT
6	404	17.3	410	1	NPRL_HUMAN
7	401.5	17.2	417	1	NPRL_MOUSE
8	355.5	15.2	412	1	GP38_HUMAN
9	310	13.3	366	1	GHSR_PIG
10	308	13.2	364	1	GHSR_RAT
11	299	12.8	366	1	GHSR_HUMAN
12	273.5	11.7	380	1	APJ_MACMU
13	272.5	11.7	380	1	APJ_HUMAN
14	267.5	11.5	377	1	APJ_MOUSE
15	263.5	11.3	444	1	OX2R_HUMAN
16	259.5	11.1	441	1	ETBR_BOVIN
17	259.5	11.1	564	1	5HT1_DROME
18	258	11.1	346	1	GALR_RAT
19	256.5	11.0	363	1	SSR3_RAT
20	255	10.9	388	1	5H4_MOUSE
21	254	10.9	348	1	GALR_MOUSE
22	253.5	10.9	444	1	OX2R_CANFA
23	252.5	10.8	444	1	SSR3_RAT
24	252	10.8	362	1	SSR3_MOUSE
25	252	10.8	395	1	TRFR_CHICK
26	250.5	10.7	398	1	TRFR_SHEEP
27	250.5	10.7	448	1	SSR3_MOUSE
28	250.5	10.7	443	1	ETBR_PIG
29	250	10.7	349	1	GALR_HUMAN
30	249.5	10.7	398	1	TRFR_HUMAN
31	249.5	10.7	427	1	ETIR_BOVIN
32	249.5	10.7	470	1	ALIA_ORYLA
33	248.5	10.6	398	1	TRFR_BOVIN

34	248.5	10.6	426	1	ETIR_RAT	P26684	rattus norv
35	248	10.6	460	1	OX2R_RAT	P56719	rattus norv
36	247.5	10.6	401	1	OPM_PIG	O95247	sus scrofa
37	247.5	10.6	412	1	TRFR_RAT	O01717	rattus norv
38	246.5	10.6	418	1	SSR3_HUMAN	P32745	homo sapien
39	245.5	10.5	427	1	ETIR_HUMAN	P25101	homo sapien
40	244.5	10.5	427	1	ETBR_COTJA	O90328	coturnix co
41	244.5	10.5	427	1	ETIR_PIG	Q29010	sus scrofa
42	244	10.5	391	1	SSRI_HUMAN	P30872	homo sapien
43	244	10.5	391	1	SSRI_MOUSE	P30873	mus musculu
44	244	10.5	391	1	SSRI_RAT	P28646	rattus norv
45	243.5	10.4	393	1	TRFR_MOUSE	P21761	mus musculu

ALIGNMENTS

RESULT 1	GP39_HUMAN	STANDARD:	PRT:	453 AA.
ID	GP39_HUMAN			
AC	043194:			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39.			
GN	GPR39.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=98110578; PubMed=9441746;			
RA	McGee K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,			
RA	Hreniuk D.L., Smith R.G., Howard A.D., Van der Ploeg L.H.T.;			
RT	"Cloning and characterization of two human G protein-coupled receptor genes (GPR38 and GPR39) related to the growth hormone secretagogue and neurotensin receptors.";			
RT	Genomics 46:426-434(1997).			
RL	-1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1 SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	EMBL: AF034633; AAC26082.1; "			
DR	GCRdb; GCR.2493; "			
DR	InterPro; IPR000276; GPCR_Rhodpsn.			
DR	Plan; PF00001; 7tm_1; 2.			
DR	PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.			
FT	DOMAIN 1	25		
FT	TRANSMEM 26	46		
FT	TRANSMEM 47	71		
FT	DOMAIN 72	92		
FT	TRANSMEM 93	109		
FT	DOMAIN 110	131		
FT	TRANSMEM 132	154		
FT	TRANSMEM 155	175		
FT	TRANSMEM 176	223		
FT	DOMAIN 224	243		
FT	TRANSMEM 244	280		
FT	DOMAIN 281	301		
FT	TRANSMEM 302	321		
FT	DOMAIN 322	347		
FT	TRANSMEM 347			

FT	DOMA:FTD	348	428	CYTOSOLASMIC (POTENTIAL).
FT	CARBOHYD	108	210	BY SIMILARITY.
FT	CARBOHYD	192	192	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	206	206	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CARBOHYD	212	212	N-LINKED (GLCNAc. . .) (POTENTIAL).
5Q	SEQUENCE	453 AA;	51328 MM;	BEA2A323420D021E CRC64;

Query Match	100.0%;	Score 2334;	DB 1;	Length 453;
Best Local Similarity	100.0%;	Pred. No. 4.7e-166;		
Matches 453; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MASPSLESGSDCSQIITIDHSHVPEFVAWIKITLIVYLIFVWGLGNSATIRTVQYLOK	60
Dd	1	MASPSLESGSDCSQIITIDHSHVPEFVAWIKITLIVYLIFVWGLGNSATIRTVQYLOK	60
QY	61	KGYLOKEVTDHMSLACSDILVFLIGMPMEFSTIIMPPLTTSYTLSCKHTLPEACST	1200
Dd	61	KGYLOKEVTDHMSLACSDILVFLIGMPMEFSTIIMPPLTTSYTLSCKHTLPEACST	1200
QY	121	ATLHVLTLSEBRYIACHPERKAAVSGPOCVKLLIGFVWTSALVALPLIFAMGTEYPL	1800
Dd	121	ATLHVLTLSEBRYIACHPERKAAVSGPOCVKLLIGFVWTSALVALPLIFAMGTEYPL	1800
QY	181	VNPSHRGLTCNRSSTRHHDEOPTSNMSICTNLSSRWTFQOSSIFGAFVYLVLLSVAF	2400
Dd	181	VNPSHRGLTCNRSSTRHHDEOPTSNMSICTNLSSRWTFQOSSIFGAFVYLVLLSVAF	2400
QY	241	MCMMNMVOLKKSQSGSLAGGRPQOLKKSSESEBRTARQOTIIFRLIYVTLVACWMPNQ	3000
Dd	241	MCMMNMVOLKKSQSGSLAGGRPQOLKKSSESEBRTARQOTIIFRLIYVTLVACWMPNQ	3000
QY	301	IRIRIIMAARKPHDWTRSYFRAYMILPLFESETEFLSSVINPLLYTVSSQOFRFVYQVLC	3600
Dd	301	IRIRIIMAARKPHDWTRSYFRAYMILPLFESETEFLSSVINPLLYTVSSQOFRFVYQVLC	3600
QY	361	CRSLQHANNEKRLRYVAHSTTDSARFVQRPPLFASRQSSARTEKIFLUSTFOSEAPQ	4200
Dd	361	CRSLQHANNEKRLRYVAHSTTDSARFVQRPPLFASRQSSARTEKIFLUSTFOSEAPQ	4200
QY	421	SKSOSLSLESTLEPNSGAKPNSAAENGFQEHV	453
Dd	421	SKSOSLSLESTLEPNSGAKPNSAAENGFQEHV	453

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CC RESULT      2
CC NTNRI_MOUSE
CC             STANDARD:          PRT;         424 AA.
CC A.00088319;
CC DT 20-AUG-2001 (Rel. 40, Created)
CC DT 20-AUG-2001 (Rel. 40, Last sequence update)
CC DT 20-AUG-2001 (Rel. 40, Last annotation update)
CC DE NEUROTENSIN RECEPTOR TYPE 1 (NT-R-1).
CC GN NTSR1 OR NTSR.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxId=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA TISSUE-Brain;
CC RA Snider J., Sano H., Ohta M.;
CC RT "Neurotensin receptor type 1.";
CC RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
CC CC -! FUNCTION: RECEPTOR FOR THE TRIDECAPEPTIDE NEUROTENSIN. IT IS
CC        ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CC        CALCIUM SECOND MESSENGER SYSTEM.
CC CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC CC HIGHEST TO TACHIKININS RECEPTORS.
CC -----
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CC EMBL, NP017027, EMB2012, 1, 5
CC

DR	MGD; MG1;97386; Ntsr.
DR	Interpro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PR00237; GPCRRHODPSN
DR	PROSITE; PS00237; G-PROTEIN_RCCEP_F1_1; 1.
DR	PROSITE; PS50262; G-PROTEIN_RCCEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Phosphorylation; Lipoprotein; Palmitate.
FT	DOMAIN 1 64
FT	TRANSMEM 65 87
FT	DOMAIN 88 96
FT	TRANSMEM 97 121
FT	DOMAIN 122 143
FT	TRANSMEM 144 165
FT	DOMAIN 166 188
FT	TRANSMEM 189 210
FT	DOMAIN 211 235
FT	TRANSMEM 236 260
FT	DOMAIN 261 308
FT	TRANSMEM 309 330
FT	DOMAIN 331 348
FT	TRANSMEM 349 372
FT	DOMAIN 373 424
FT	CARBOHYD 4 4
FT	CARBOHYD 38 38
FT	CARBOHYD 42 42
FT	CARBOHYD 211 211
FT	DISULFID 141 224
FT	LIPID 388
SO	SEQUENCE 424 AA; 47216 MW; BE9A723171A4871A CRC64;

Query Match	20.6%;	Score 481.5;	DB 1;	Length 424;
Best Local Similarity	29.3%;	Pred. No. 9.1e-29;		
Matches 123;	Conservative 73;	Mismatches 165;	Indels 59;	Gaps 9;

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QY      8 GSPCQIDHSHVPEEVAATMKTLLVYLILFVWGLDNGSMTIKWYOVULOKEKY--110 65
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      41 GNSSESLPEKNSMDVNTDIYSKVLATVATLAFVYGVGNSTY--AFLTARKKSLOSQ 98

QY      66 KETDMDVMSIACSDILVFLIMPMEFEYSIIMNPLTSSVYLSCKLTTELFEACSYATLLH 125
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      99 SYTHYHLSLALSDLLILLILMLAMPVLEINFLWYHNHPAFGAGRGVYFLRACGYATALN 155

QY      126 VLTLSERYIALICHPRPKAVSGECQYKLLIGVWYTSALVALPLLFAMGEYELVNPVS 185
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      159 VASLSYERIALICHPFKAKTMTSMRSRTRKEISAIWLASLALVALVPMLEFTGID----- 210

QY      186 HRLJLONRSTHNEHPETSMSICT---NLSRKNVYFQSSIFGAFVUYLVLLSVAFMC 242
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      211 -----NRSDAQH-----PGGLVCTPVTATVATKVVIVQVNTFMSEFLPMILSLNTVI 255

QY      243 WNMQVYL---KSGKSLAGTRPRPOLRKSESBSRT-----ARROTIFLRL 287
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      260 ANKLITMVAHQAAEQRGVCTYGTGTH-----NSLEHSTNMSLTEGRQALRHGVLYIRA 312

QY      288 IYVTLAVCMMPNOIRIIMAAAKPRKHDWTRSYFRAYMILLPSETEFEYLSVINPLTAVS 347
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      313 VVIAFVYCVCLPRYHAKRLMFCITSDEQMTTLLPFDYHYFMILNALFVYSSAINPLINLV 372

QY      348 SQQFRREVQVYLCSRLSDQAHNHEKRLVHAHSTDSARFVQRPLLFASRQSSARTEK 407
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      373 SANFRQVFLSTLACLCPCQWRRRRKKR-----PFSKRPMMSMSNNAFSSATRE 421

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ID	NTRI_RAT	STANDARD;	PRT;	424 AA.
NT	NTRI_RAT			
AC	P20769;			
DT	01-FEB-1991 (Rel. 17, Created)			
DT	01-FEB-1991 (Rel. 17, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	NEUROTENSIN RECEPTOR TYPE 1 (NT-R-1) (HIGH-AFFINITY LEVOACASTINE-SENSITIVE NEUROTENSIN RECEPTOR) (NTRH).			
GN	NTSR1.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murineae; Rattus			
OX	[NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=90297956; PubMed=1694443;			
RA	Tanaka K., Masu M., Nakanishi S.;			
RT	"Structure and functional expression of the cloned rat neurotensin receptor.";			
RT	Neuron 4:847-854(1990).			
CC	- FUNCTION: RECEPTOR FOR THE TRIDEAPEPTIDE NEUROTENSIN. IT IS ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.			
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	HIGHEST TO TACHIKININS RECEPTORS.			
DR	PIR: JH0164; JH0164.			
DR	GCRDB: GCR 0219; -;			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm1_1; 1.			
DR	PRINTS: PR00237; GPCRHDOPSN.			
DR	PROSITE: PS00237; G-PROTEIN_RECEP_FL1; 1.			
DR	PROSITE: PS00262; G-PROTEIN_RECEP_FL2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	phosphorylation; Lipoprotein; Palmitate.			
FT	DOMAIN	1	64	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	65	87	1 (POTENTIAL).
FT	DOMAIN	88	96	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	97	121	2 (POTENTIAL).
FT	DOMAIN	122	143	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	144	165	3 (POTENTIAL).
FT	DOMAIN	166	188	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	189	210	4 (POTENTIAL).
FT	DOMAIN	211	235	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	236	260	5 (POTENTIAL).
FT	DOMAIN	261	308	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	309	330	6 (POTENTIAL).
FT	DOMAIN	331	348	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	349	372	7 (POTENTIAL).
FT	DOMAIN	373	424	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	4	4	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	38	38	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	42	42	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID	142	225	BY SIMILARITY.
FT	LIPID	388	388	PALMITATE (POTENTIAL).
SO	SEQUENCE	424 AA;	47054 MW;	A9C2P7EAFB9BCD3 CRC64;

[illegible]

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Db      182  SRSTKFKFISAIWLASALLAIPLMFLTMGLQ-----NFGSDGTH-----PGG 222
Oy      208  SICINLSSRMT---VPOSSIFGAIIVVLLVLLSAYFQCMNMKQYLM--KKGKSLA---- 258
      223  LVCPRIVDTAIVKVVIVQVNEFMSPLEPMLVLSINLTIVANKLVYHQAEQGRVCTGT 282
Db      259  -GGRPEOLRKSESESESRATAROTIIFLRILVYLVAICWMPNOIKRIIMAAKPRHWDTRS 317
Oy      283  HNGLEHSTFNMTIEPRGVQALRHGVLLVRAVLVAIFVQWCIPEYHVRILMFCYISDEQWTF 342
Db      318  YFRAYMILPPESEFFFLSVSTINPLLTVSSQGRFVQVYOLCRLSLQIANHEKRLRVH 377
Oy      343  LFEDYHYFYMTNLAFVSSAINILVLNVLSANRQVFLSTLACLCPGMRHRRKKR---- 398
Db      378  AHSFTDSARFVORPLLPASROSSARRTK 407
Oy      399  -----PTFSRKRNMSMSNNAFSTSATRE 421

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	RESULT	4
ID	NTR1_HUMAN	STANDARD; PRT; 418 AA.
AC	P30989;	
DT	01-JUL-1993 (Rel. 26, Created)	
DT	01-JUL-1993 (Rel. 26, Last sequence update)	
DT	20-AUG-2001 (Rel. 40, Last annotation update)	
DE	NEURENENSIN RECEPTOR TYPE 1 (NT-R1) (HIGH-AFFINITY LEVOCABASTINE-INSENSITIVE NEURENENSIN RECEPTOR) (NTRH).	
GN	NTR1 OR NTRR.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	NCBI_Taxid=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=93154505; PubMed=8381365;	
RA	Vita N., Laurent P., Lefort S., Chalou P., Dumont X., Kaghad M.,	
RA	Gully D., Le Fur G., Ferrara P., Capit D.;	
RT	"Cloning and expression of a complementary DNA encoding a high	
RT	affinity human neurensin receptor.";	
RL	FESL Lett. 317:139-142(1993).	
CC	-I- FUNCTION: RECEPTOR FOR THE TRIDECAPETIDE NEURENENSIN. IT IS ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.	
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.	
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. HIGHEST TO TACHYKININS RECEPTORS.	
CC	-----	
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CC	or send an email to license@isb-sib.ch .	
DR	EMBL; X70070; CAA49675.1; -.	
DR	PIR; S29506; S29506.	
DR	GCRDB; GCR_0577; -.	
DR	GCRDB; GCR_2067; -.	
DR	MIM; 162651; -.	
DR	InterPro; IPR000276; GPCR_Rhodpsn.	
DR	Pfam; PF00001; 7tm_1; 1.	
DR	PROSITE; PS00237; G_PROTEIN_RECPE_F1.1; 1.	
DR	PROSITE; PS50262; G_PROTEIN_RECPE_F1.2; 1.	
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;	
KW	Phosphorylation; Lipoprotein; Palmitate.	
FT	DOMAIN 1 63	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 64 86	1 (POTENTIAL).
FT	DOMAIN 87 95	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 96 120	2 (POTENTIAL).
FT	DOMAIN 121 142	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 143 164	3 (POTENTIAL).


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CC EMBL: U51908; AAB17285.1; -
DR MGD: MGI:108018; Ntstr2.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 2.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Lipoprotein; Palmitate.
FT DOMAIN 1 32
FT TRANSMEM 33 55
FT DOMAIN 56 64
FT TRANSMEM 65 87
FT DOMAIN 88 109
FT TRANSMEM 110 131
FT DOMAIN 132 154
FT TRANSMEM 155 176
FT DOMAIN 177 217
FT TRANSMEM 218 238
FT DOMAIN 239 298
FT TRANSMEM 299 319
FT DOMAIN 320 338
FT TRANSMEM 339 359
FT DOMAIN 360 417
FT DISULFID 108 194
FT LIPID 378
SQ SEQUENCE 417 AA; 46537 MW; EBFDDBD6507223DD CRC64;

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Query Match 17.2%; Score 401.5; DB 1; Length 417;
Best Local Similarity 26.9%; Pred. No. 7,6e-23;
Matches 101; Conservative 68; Mismatches 133; Indels 73; Gaps 8;

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OY 28 WITTLILVILVFNGLNSATIRVLOKKGVLQKEVDHMYSLACSDILVFLIGM 87
DB 30 WAKVETAYKSLIFALGTGNALSVHY--VLAKEGRPRGRKXHYSLASLLILLISY 87
OY 88 PMEFSIIMNPLTSSYTLCKLHFLPACSAVALLVLLTSFERYIALCHPFRYKAVS 147
DB 88 PMELYNEVSHYPMVFGDLCRGYFVRELCAVAVLASAERCLAVCQPLRARILL 147
OY 148 GPCQVALLIGFWVTALVALPLLPAMGTEYPLVNVPSHRGLTCNRSSRHHEQPTSM 207
DB 148 TPRRTRELTLVWVASLGLAPMAVIMGQKHEM-----BRADGEDEPAS- 191
OY 208 SICTNLSR-----WTFQSSIFGAFVYLVLLS----- 237
DB 192 RCTTVLVSRASSSTQVRAGLIRSPMLRL--TAILNGITVNHVALVLSQVVSASQVNS 250
OY 238 -----VAFMCNMNQVLKMSQKSLAGSTRPPOLRKSSESESRARQTIIF 284
DB 251 IPRRLBLSEBGLIGITM-----RKTLSLGVQASIVRHKDAQSIRSLQNSAQV- 299
OY 285 LRLIVVTLAVCMNPNOIRKIMAAAKPKHMDTRSYFRAYVILLPFSTFYLSVINPLLY 344
DB 300 LRAIVAVVYICWLPYHARKLMCTIIPDDGTDLDYHYFYVWTVTLFVSSAVTPVLY 359
OY 345 TVSSQOFRFRFVQVL 359
DB 360 NAVSSSFRLFLLESL 374

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RESULT 8
GP38 HUMAN STANDARD; PRT; 412 AA.
AC 043193;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR38.
GN GPR38
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=9441746;
RX MEDLINE=98110578;
RA Hreniuk K.K., Tan C.P., Palyha O.C., Liu J., Feighner S.D.,
RA Hreniuk D.L., Smath R.G., Howard A.D., van der Ploeg L.H.T.;
RT "Cloning and characterization of two human G protein-coupled receptor
RT genes (GPR38 and GPR39) related to the growth hormone secretagogue
RT and neurotensin receptors."
RL Genomics 46:426-434(1997).
CC -1- SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THYROID, STOMACH, AND BONE
CC MARROW.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF034632; AAC26081.1; -
DR GCRDB: GCR_2494; -
DR MIM: 602885; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 2.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT DOMAIN 57 74
FT TRANSMEM 75 94
FT DOMAIN 95 112
FT TRANSMEM 113 134
FT DOMAIN 135 157
FT TRANSMEM 158 178
FT DOMAIN 179 246
FT TRANSMEM 247 270
FT DOMAIN 271 298
FT TRANSMEM 299 320
FT DOMAIN 321 334
FT TRANSMEM 335 358
FT DOMAIN 359 412
FT DISULFID 111 235
FT CARBOHYD 6
FT CARBOHYD 192
SQ SEQUENCE 412 AA; 45344 MW; C13FF6165012DER3 CRC64;

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Query Match 15.2%; Score 355.5; DB 1; Length 412;
Best Local Similarity 28.5%; Pred. No. 1,9e-19;
Matches 111; Conservative 65; Mismatches 169; Indels 45; Gaps 13;

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OY 4 PSLGSD---CSQIIDSHVPEFVATWIKTLVLIIFVWGLNSATIRVLOK 60
DB 20 PALPCDERRCS-----PPLGALVPT--AVCLCLFVGVSSNVVTV--MLGR 65
OY 61 KGYLOKEVTDHNVSLACSDILVFLGMPMEFYSTIMPLTSSYTLCKLHFLFEACSY 120
DB 66 YRDMKTTNLTLSGMAVSDLLI-LGLPLDLYR-LMSRPVFPGLLCRLSLVYGECTY 123
OY 121 ATLHLVTLSEERYIALCHPFRYKAVSGPCOVKLLIFFWVTALVALPLLPAMGTEY-P 179
DB 124 ATLHLMTLSVEREYIALCHPRLARVLTTRRRVALVLAVALLSAGPLFLVGVQDP 183
OY 180 LVN-VPSHRGLTCNRSSRHHEQ-----PETSNNSTCTNLSRMTVQSS 223
DB 184 GISVPGINGTARIASSPLASPLMLSRAPPSPSGPETAALALFSRECRPSAQ-- 241

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QY	224	IFGAVVYVILLVSVAAQCMNMAMVKKSGSLAGTSPDPLRKSSSESRNAROTII	283
Db	242	- LGLALRWMLWMTAYTAFELPLFCISILGLIGRELMSRRP - LRGPASGREGKHOTVR	296
QY	284	FLRLIVTLAVCMQPNQIRIRMAAKPKHDWTRSYFRAYMILLPFSEFFYLSVNPDL	343
Db	299	VLLAVVLAFTICWLPFHVGRITV - NTEDSRMYFSQYFNIVALQ - LFLYSASINDIL	354
OY	344	YTVSSQFRRVFOVYLCRLSLCHANEKR	373
Db	355	YNIISKRYRAAFAKLLLRKSRPRGRHSR	384

RESULT 9

ID	GHSR_PIG	STANDARD:	PRT:	366 AA.
AC	Q95254; Q95255;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DT	GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1 (GHS-R) (GH-RELEASING PEPTIDE RECEPTOR) (GHRP).			
GN	GHSR.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCBI_TaxID=9823;			
RY	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-YORKSHIRE; TISSUE-Pituitary;			
RC	MEDLINE=96337998; PubMed=8688086;			
RA	Howard A.D., Feiginger S.D., Cully D.F., Arena J.P.,			
RA	Liberator P.A., Rosenblum C.I., Hamelin M., Hrenluk D.L.,			
RA	Palya O.C., Anderson J., Parese P.S., Diaz C., Chou M.,			
RA	McGee K.K., Gong S.-S., Chaudh L.-Y., Elbrecht A., Deshvez M.,			
RA	Heavens R., Rigby M., Srinathsinghji D.J.S., Dean D.C., Mellito D.G.,			
RA	Patchett J.M., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K.,			
RT	Schaeffer J.M., Smith R.G., van der Ploeg L.H.T.;			
RT	"A receptor in pituitary and hypothalamus that functions in growth hormone release.";			
RL	Science 273:974-977(1996).			
CC	-1- FUNCTION: RECEPTOR FOR GROWTH HORMONE RELEASING PEPTIDES (GHRP) AS WELL AS NON-PEPTIDE. LOW MOLECULAR WEIGHT SECRETAGOGUES (E.G. L-692,429, MK-0677). THIS RECEPTOR IS COUPLED TO G-ALPHA-11			
CC	PROTEIN. BINDING POTENCY FOR THE SECRETAGOGUES IS IN THE ORDER: MK-0677 > GHRP-2 > GHRP-6.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1A (SHOWN HERE) AND 1B; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 1B APPEARS NOT TO BIND SECRETAGOGUES.			
CC	-1- TISSUE SPECIFICITY: PITUITARY AND HYPOTHALAMUS.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; U60178; AAC48630.1; -;			
DR	EMBL; U60180; AAC48631.1; -;			
DR	GCRdb; GCR_1539; -;			
DR	GCRdb; GCR_1539; -;			
DR	InterPro; IPR003905; GHSR_receptor.			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.			
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.			
DR	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Alternative splicing.			

FT	DOMAIN	1	40	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	41	66	1 (POTENTIAL).
FT	DOMAIN	67	72	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	73	96	2 (POTENTIAL).
FT	DOMAIN	97	117	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	118	139	3 (POTENTIAL).
FT	DOMAIN	140	162	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	163	183	4 (POTENTIAL).
FT	DOMAIN	184	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	212	235	5 (POTENTIAL).
FT	DOMAIN	236	263	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	264	285	6 (POTENTIAL).
FT	DOMAIN	286	302	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	303	326	7 (POTENTIAL).
FT	DOMAIN	327	366	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	116	198	BY SIMILARITY.
FT	CARBOHYD	13	13	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	27	27	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	26	289	AAVAFELICWLPFHVGRKLSK -> GGSOCALIELSLRGC
FT	VARSPPLIC			PHSSLCFSPSP (IN ISOFORM 1B).
FT	VARSPPLIC			MISSING (IN ISOFORM 1B).
FT	VARSPPLIC	290	366	MISSING (IN ISOFORM 1B).
SEQ	SEQUENCE	366 AA:	41194 MN:	2C850B3EF61B7C1C CR064:

Query Match	13.3%;	Score 310;	DB 1;	Length 366;
Best Local Similarity	27.8%;	Pred. NO. 4e-16;		
Matches	95;	Conservative	68;	Mismatches 139;
				Indels 40;
				Gaps 12;

QY	20	VPEEVAATWIKITLLIIVYLIIIFWGLIGLSNATIRYQVLOKKGYLOKEVTDHMTSLACSD	79
Db <td>35</td> <td>LPDPPTLLAGVATCYAL--FVVGAGINGLIILVYSRRE---MTTINLYLSSMASTD</td> <td>89</td>	35	LPDPPTLLAGVATCYAL--FVVGAGINGLIILVYSRRE---MTTINLYLSSMASTD	89
QY <td>80</td> <td>ILVFLIGMPMEFYSIINNPITTSYTLISCKLHTEFEACSVATLHVLTLSERYIAICH</td> <td>139</td>	80	ILVFLIGMPMEFYSIINNPITTSYTLISCKLHTEFEACSVATLHVLTLSERYIAICH	139
Db <td>90</td> <td>ILILFLC-MPDLIFR-LWQYRPWNLGNLCKLQFVSESCSYATVLTITALLSYERFYAICF</td> <td>147</td>	90	ILILFLC-MPDLIFR-LWQYRPWNLGNLCKLQFVSESCSYATVLTITALLSYERFYAICF	147
QY <td>140</td> <td>PPRKANSGPCQVYLLIGFWYMSALVALPLFLMGTGEPDIAVWPBHRLLTGNRSSTRHH</td> <td>199</td>	140	PPRKANSGPCQVYLLIGFWYMSALVALPLFLMGTGEPDIAVWPBHRLLTGNRSSTRHH	199
Db <td>148</td> <td>PLRAVAVYTKRVRKVLVLIIVMAAFGASGIFVYLVGVEHD-----NGDDPRPT</td> <td>195</td>	148	PLRAVAVYTKRVRKVLVLIIVMAAFGASGIFVYLVGVEHD-----NGDDPRPT	195
QY <td>200</td> <td>EOPERSNNSICTNLSRHWTFPOSSIFCAFVYV-LVYLIVSAFMCMMMOVLKKSQGSILA</td> <td>258</td>	200	EOPERSNNSICTNLSRHWTFPOSSIFCAFVYV-LVYLIVSAFMCMMMOVLKKSQGSILA	258
Db <td>196</td> <td>NECRATERAVASGLLT-VMMVSSVFEFFLPVFCULVYLSL-----IGRLWRRKGEAA</td> <td>248</td>	196	NECRATERAVASGLLT-VMMVSSVFEFFLPVFCULVYLSL-----IGRLWRRKGEAA	248
QY <td>259</td> <td>GSTRPOLRKSESEBSERTARRQTIITFLRLVYLIVLAVGMNMQNRIIRLMAAAKPKHDWTR-S</td> <td>317</td>	259	GSTRPOLRKSESEBSERTARRQTIITFLRLVYLIVLAVGMNMQNRIIRLMAAAKPKHDWTR-S	317
Db <td>249</td> <td>VGS---SLRDQN-----HKQYTKMLAVYVFAFLICWLFPHGRLLFSKSLGPGSVEIA</td> <td>298</td>	249	VGS---SLRDQN-----HKQYTKMLAVYVFAFLICWLFPHGRLLFSKSLGPGSVEIA	298
QY <td>318</td> <td>YFRAYMILLPSETEFFYLSVINYINPLATVVSQOFRFRVYOVVL</td> <td>359</td>	318	YFRAYMILLPSETEFFYLSVINYINPLATVVSQOFRFRVYOVVL	359
Db <td>299</td> <td>QISQYCNLYSF--VLFTLSAINDIILINMSKKRYRAVFKLL</td> <td>338</td>	299	QISQYCNLYSF--VLFTLSAINDIILINMSKKRYRAVFKLL	338
RESULT	10		
GHSR_RAT			
ID	GHSR_RAT	STANDARD;	PRT; 364 AA.
AC	008725:		
DT	15-JUL-1998	(Rel. 36, Created)	
DT	15-JUL-1998	(Rel. 36, Last sequence update)	
DT	30-MAY-2000	(Rel. 39, Last annotation update)	
DE	GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1 (GHS-R) (GH-RELEASING		
GN	PEPTIDE RECEPTOR) (GHR).		
GN	GHSR.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=pituitary;		
RX	MEDLINE=97246555; PubMed=9092793;		
RA	McKee K.K., Palyha O.C., Feigelson S.D., Hreniuk D.L., Tan C., Phillips M.S., Smith R.G., der Ploeg L.H.T., Howard A.D.;		

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RT "Molecular analysis of rat pituitary and hypothalamic growth hormone secretagogue receptors." ;
RL Mol. Endocrinol. 11:415-423(1997).
RP SEQUENCE OF 1-240 FROM N.A. STRAIN-WISTAR; TISSUE=pituitary; MEDLINE=98100386; PubMed=9437732; Yokote R., Sato M., Matsubara S., Ohye H., Niml M., Murao K., Takahara J.;
RA "Molecular cloning and gene expression of growth hormone-releasing peptide receptor in rat tissues.";
RL Peptides 19:15-20(1998).
CC -I FUNCTION: RECEPTOR FOR GROWTH HORMONE RELEASING PEPTIDES (GHRP) AS WELL AS NON-PEPTIDE, LOW MOLECULAR WEIGHT SECRETAGOGES (E.G. L-692,459, MK-0677). THIS RECEPTOR IS COUPLED TO G-ALPHA-11 PROTEINS. (BY SIMILARITY).
CC -I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
DR EMBL: U94321; AAC53156.1; -.
DR EMBL: AB001982; BAA21777.1; ALU_INIT.
DR GCRDb: GCR 1383; -.
DR InterPro: IPR003905; GHSL_receptor.
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCRRHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR G-Protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 41 66 1 (POTENTIAL).
FT DOMAIN 67 72 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 73 96 2 (POTENTIAL).
FT DOMAIN 97 117 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 118 139 3 (POTENTIAL).
FT DOMAIN 140 162 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 163 183 4 (POTENTIAL).
FT DOMAIN 184 211 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 212 235 5 (POTENTIAL).
FT DOMAIN 236 263 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 264 285 6 (POTENTIAL).
FT DOMAIN 286 302 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 303 326 7 (POTENTIAL).
FT DOMAIN 327 364 CYTOPLASMIC (POTENTIAL).
FT DISULFID 115 197 BY SIMILARITY.
FT CARBOHD 113 13 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHD 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 364 AA; 40963 MW; DCBF559BE061EEE9 CRC64;

Query Match 13.2%; Score 308; DB 1; Length 364;
Best Local Similarity 26.5%; Pred. No. 5.7e-16;
Matches 96; Conservative 71; Mismatches 137; Indels 58; Gaps 133;

OY 7 PGSDCSQIIDSHPVEEFVATWIKITLLIVYLIFVMGLSGSATIRTVQLVKRGYLOK 66
DB ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Dd 24 PGNDS--LPBELLPLFPAPPLAGTAICVAL--FYVGISGLMLIMLVSRRE---LRT 75

OY 67 EVTDHMSVLACSDILVELIGMPMEFYSTINNELTSSYTLSCKHTEFLFEACSVATLIHV 126
DB ::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Dd 76 TTNTLYLSMAFSDELIFLC-MPLDLVR-TMWQRPWNFDLCKLFQFVSSECTAYATVLTII 133

OY 127 LTLESPIATICHPPRYAVSPCOOVKLLIGVWTSALVALLPLFAAGTEPLVNVESH 186
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Dd 134 TALSYERFALCFIPRAKVVTYTKGRVKVILLIVYAVACSAGPIPVLVGVHEH----- 186

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OY      187 RGLTGNSSSRHHEDQETSNMISCTVLSRMTVFQSGIFGAFVIVLVLTSLVAFCMNMM 246
DB      187 -----NSTDTRDINECRATEFANRSGLLT-VWVVSSVFPLEPFCILTVL-----YSLI 234
OY      247 QVLMSKQSGSLAGGTBPOLRKSESESESTARRQTIIFLRLIVTLAVLCWMPNOIRIMA 306
DB      235 GRKLMMRRGRGAAGA---SLRDQN-----HKQIVKMALVVAFFILCMLPFHVGRYL- 283
OY      307 AAKKHMTSY-----FRAYILLPEETFEFFLYSSINPLTVSSQQPRFRFYQ 357
DB      284 -----FSKSFEPSGLEIAIQSCNVLSF--VLFYSAAINPLVNMISKRYRAVFR 334
OY      358 VL 359
DB      :|
DB      335 LL 336

RESULT 11
GHSR_HUMAN
ID GHSR_HUMAN STANDARD: PRT: 366 AA.
AC O92847; O92848;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GROWTH HORMONE SECRETAGOGUE RECEPTOR TYPE 1 (GHS-R) (GH-RELEASING PEPTIDE RECEPTOR) (GHRP).
CN GHSR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=96337998; PubMed=8688086;
RA Howard A.D., Reigner S.D., Cully D.F., Arena J.P., Liberator P.A., Rosenblum C.I., Hamelin M., Hrenluk D.L., Palaya O.C., Anderson J., Pares P.S., Diaz C., Chou M., Liu K.K., McKee K.K., Pong S.-S., Chang L.-Y., Elbrecht A., Daskiewicz M., Rahearts A.A., Nargund R., Griffin P.R., Demartino J.A., Gupta S.K., Schaeffer J.M., Smith R.G., van der Pleeg L.H.T.;
RA "A receptor in pituitary and hypothalamus that functions in growth hormone release."
RL Science 273:974-977(1996).
CC CC
CC -I- FUNCTION: RECEPTOR FOR GROWTH HORMONE RELEASING PEPTIDES (GHRP) AS WELL AS NON-PEPTIDE, LOW MOLECULAR WEIGHT SECRETAGOGUES (E.G. L-692,429, MK-0677). THIS RECEPTOR IS COUPLED TO G-ALPHA-11 PROTEINS. POTENCY RANKING FOR SECRETAGOGUE INHIBITION IS MK-0677 > GHRP-2 > GHRP-6.
CC CC
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1A (SHOWN HERE) AND 1B; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM 1B APPEARS NOT TO BIND SECRETAGOGUES.
CC CC
CC -I- TISSUE SPECIFICITY: PITUITARY AND HYPOTHALAMUS.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC CC
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CC CC
CC -----
EMBL: U60179; AAC50653.1; -.
DR EMBL: U60181; AAC50654.1; -.
DR GCRDB: GCR_1917; -.
DR GCRDB: GCR_1918; -.
DR MIM: 601896; -.
DR InterPro: IPR003905; GHS1_receptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.

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Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHHODPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_FL_1; 1.
 DR PROSITE: PS50262; G_PROTEIN_RECIP_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; glycoprotein;
 Alternative splicing.
 FT DOMAIN 1 40
 FT TRANSSEM 41 66
 FT TRANSSEM 67 72
 FT TRANSSEM 73 96
 FT TRANSSEM 97 117
 FT TRANSSEM 118 139
 FT TRANSSEM 140 162
 FT TRANSSEM 163 183
 FT TRANSSEM 184 211
 FT TRANSSEM 212 235
 FT TRANSSEM 236 263
 FT TRANSSEM 264 285
 FT TRANSSEM 302 326
 FT TRANSSEM 327 366
 FT TRANSSEM 367 398
 FT TRANSSEM 399 430
 FT TRANSSEM 431 462
 FT TRANSSEM 463 494
 FT TRANSSEM 495 526
 FT TRANSSEM 527 558
 FT TRANSSEM 559 590
 FT TRANSSEM 591 622
 FT TRANSSEM 623 654
 FT TRANSSEM 655 686
 FT TRANSSEM 687 718
 FT TRANSSEM 719 750
 FT TRANSSEM 751 782
 FT TRANSSEM 783 814
 FT TRANSSEM 815 846
 FT TRANSSEM 847 878
 FT TRANSSEM 879 910
 FT TRANSSEM 911 942
 FT TRANSSEM 943 974
 FT TRANSSEM 975 1006
 FT TRANSSEM 1007 1038
 FT TRANSSEM 1039 1070
 FT TRANSSEM 1071 1102
 FT TRANSSEM 1103 1134
 FT TRANSSEM 1135 1166
 FT TRANSSEM 1167 1198
 FT TRANSSEM 1199 1230
 FT TRANSSEM 1231 1262
 FT TRANSSEM 1263 1294
 FT TRANSSEM 1295 1326
 FT TRANSSEM 1327 1358
 FT TRANSSEM 1359 1390
 FT TRANSSEM 1391 1422
 FT TRANSSEM 1423 1454
 FT TRANSSEM 1455 1486
 FT TRANSSEM 1487 1518
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Db 257 FALCAMPYHLVKTLYMGSLLHWPCEDFLFMANVFPYCICISYVNSCLNPLFLYAFDPFR 316
OY 352 RRVEVOYLCC 361
Db 317 ROACTSMGCC 326

RESULT 13
APJ_HUMAN STANDARD; PRT; 380 AA.
ID APJ_HUMAN
AC P35414;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, last sequence update)
DT 20-AUG-2001 (Rel. 40, last annotation update)
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GN AGTRL1 OR APJ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94124031; PubMed=8294032;
RA O'Dowd B.F., Heiber M., Chan A., Heng H.H., Tsui L.-C., Kennedy J.L.,
RA Shi X., Petronis A., George S.R., Nguyen T.;
RT "A human gene that shows identity with the gene encoding the
RT angiotensin receptor is located on chromosome 11."
RL Gene 136:355-360(1993).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHLY RELATED TO ANGIOTENSIN RECEPTOR 1.
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DR EMBL: U03642; AAA18954.1; -
DR GCRdb; GCR_0806; -
DR MIM: 600052; -
DR InterPro: IPR003904; APJ_rcptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PRO0001; 7tm_1.1.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
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FT TRANSMEM 27 51
FT TRANSMEM 52 66
FT TRANSMEM 67 91
FT DOMAIN 92 100
FT TRANSMEM 101 125
FT DOMAIN 126 144
FT TRANSMEM 145 166
FT DOMAIN 167 200
FT TRANSMEM 201 221
FT TRANSMEM 222 244
FT TRANSMEM 245 271
FT TRANSMEM 272 284
FT DOMAIN 285 308
FT TRANSMEM 309 380
FT DOMAIN 380 380
FT CARBOHYD 15
FT CARBOHYD 175
FT SEQUENCE 380 AA; 42660 MW; 78DB18BEA6D2B2E4 CRC64;
SQ

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Best Local Similarity 24.6%; Pred. No. 2,5e-13;
Matches 91; Conservative 62; Mismatches 154; Indels 63; Gaps 14;

OY 8 GSDCSQIIDHSHVPEEVAWIKITLIL--VLLIFVGLGNSATIRVQVLRKQYQ 65
Db 4 GGDFFNYGADNOSCEYTDWKSSCALIPALYMLVFLGTTGNGVL--WVFRSREKR 61
OY 66 KEVTHMWSLACSDILVLLIGMPMEFYSLINPLTSSY-----TLCKLTFEPCASY 120
Db 62 KSDADIFLASLAVAD-LTEVVTLP-----LMATYTRDWDMPGTFCKLSSYLIFVNM 114
OY 121 ATLLHVLTFSEFYTAICHP-----FRYKAVGPCQVLLIGFWTSALVALPLPAMG 175
Db 115 ASVPELTGSLPDRYLAIRPANNALRLR-VSGAVATVVL-----WVLAALLAMVAV-LR 168
OY 176 TEYPLVNPVSHRGILTCNRSSTRHEDPETSMMSCITNLSRMT---VFOSSIGFAPVY 231
Db 169 TTGDELENTTK--VQC-----YNDYSMAVATVSEMAVEGVGSSTVVGHVVP 213
OY 222 LVLLSVAFMCMNMVQLMKSGKSLAGTRPPQLRKSSESESTARROTIFLRLLVPT 291
Db 214 FTIMLTCTFFET-----AQTIAHFR-----KERIEGLKRRRLISTIVLVPT 256
OY 292 LAVCMPPNQIRIMAAAKPKHDWTRSYRAYVILIPSEFPYLSYINPLLYTVSSQCF 351
Db 257 FALCAMPYHLVKTLYMGSLLHWPCEDFLFMANVFPYCICISYVNSCLNPLFLYAFDPFR 316
OY 352 RRVEVOYLCC 361
Db 317 ROACTSMGCC 326

RESULT 14
APJ_MOUSE STANDARD; PRT; 377 AA.
ID APJ_MOUSE
AC Q9WV08;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, last sequence update)
DT 20-AUG-2001 (Rel. 40, last annotation update)
DE PROBABLE G-PROTEIN-COUPLED RECEPTOR APJ (MSR).
GN AGTRL1 OR APJ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Rizzoci K.;
RT "The G protein-coupled receptor msr/APJ is expressed in endothelial
RT precursors."
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL: AJ007612; CAB50696.1; -
DR MGD: MGI1346086; Agtrl1.
DR InterPro: IPR003904; APJ_rcptor.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1.1.
DR PRINTS: PRO0237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 24
SQ

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Query Match 11.7%; Score 272.5; DB 1; Length 380;

Db 354 YANSAMPITYNFIISGKFRFEFKAFSCCIGVHHROEDRI-TR----- 396
QY 393 LFAERROSSARTEKIFLSTPQSEAEPOSKOSLSLESPNSGAKP 439
Db 397 --GRTSTESRKSILTTOISNFDNISLSQVYLTSTLPAANGAP 440

Search completed: January 8, 2002, 23:10:35
Job time: 385 sec